

1683

P#20



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/469,200D

DATE: 11/18/2002

TIME: 13:01:24

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\11182002\I469200D.raw

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NOV 29 2002

TECH CENTER 1600/2900

3 <110> APPLICANT: Weigel, Paul H.  
4 DeAngelis, Paul  
5 Kumari, Kshama  
7 <120> TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof  
9 <130> FILE REFERENCE: 3554.011  
11 <140> CURRENT APPLICATION NUMBER: US 09/469,200D  
12 <141> CURRENT FILING DATE: 1999-12-21  
14 <150> PRIOR APPLICATION NUMBER: US 09/178,851  
15 <151> PRIOR FILING DATE: 1998-10-26  
17 <150> PRIOR APPLICATION NUMBER: US 60/064,435  
18 <151> PRIOR FILING DATE: 1997-10-31  
20 <160> NUMBER OF SEQ ID NOS: 10  
22 <170> SOFTWARE: PatentIn version 3.1  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 1254  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Streptococcus equisimilis  
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32 atttacgtca atgtttatct ctttggtgct aaaggaagct tgtcaattta tggttttttg 120  
34 ctgatatgctt acctattagt caaaatgtcc ttatcctttt ttacaagcc atttaaggga 180  
36 agggctgggc aatataaggt tgcagccatt attcctctt ataacgaaga tgctgagtca 240  
38 ttgctagaga ccttaaaaag tgttcagcag caaacctatc ccctagcaga aatttatggt 300  
40 gttgacgatg gaagtgtgta tgagacaggt attaagcgca ttgaagacta tgtgcgtgac 360  
42 actggtgacc tatcaagcaa tgtcattggt catcggtcag agaaaaatca aggaaagcgt 420  
44 catgcacagg cctgggcctt tgaaagatca gacgctgatg tctttttgac cgttgactca 480  
46 gatacttata tctaccctga tgccttagag gagttgttaa aaaccttta tgaccaact 540  
48 gtttttgctg cgacgggtca ccttaatgtc agaaatagac aaaccaatct cttaacacgc 600  
50 ttgacagata ttcgctatga taatgctttt ggcgttgaa gagctgcca atccgttaca 660  
52 ggtaatatcc ttgtttgctc aggtccgctt agcgtttaca gacgagagg gtgtgttcct 720  
54 aacatagata gatacatcaa ccagacctc ctgggtattc ctgtaagtat tggatgatgac 780  
56 aggtgcttga ccaactatgc aactgattta ggaaagactg tttatcaatc cactgctaaa 840  
58 tgtattacag atgttcctga caagatgtct acttacttga agcagcaaaa ccgctggaac 900  
60 aagtccttct ttagagagtc cattatttct gttaaagaaa tcatgaacaa tccttttgta 960  
62 gccctatgga ccatacttga ggtgtctatg tttatgatgc ttgtttatc tgtggtggat 1020  
64 ttcttttgta gcaatgtcag agaatttgat ttgtcaggg ttttagcctt tctggtgatt 1080  
66 atcttcattg ttgccctgtg tcggaacatt cattacatgc ttaagcacc gctgtccttc 1140  
68 ttgttatctc cgttttatgg ggtgctgcac ttgtttgtcc tacagccctt gaaattatat 1200  
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73 <210> SEQ ID NO: 2  
74 <211> LENGTH: 417  
75 <212> TYPE: PRT  
76 <213> ORGANISM: Streptococcus Equisimilis

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78 &lt;400&gt; SEQUENCE: 2

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80 Met Arg Thr Leu Lys Asn Leu Ile Thr Val Val Ala Phe Ser Ile Phe
81 1      5      10      15
84 Trp Val Leu Leu Ile Tyr Val Asn Val Tyr Leu Phe Gly Ala Lys Gly
85      20      25      30
88 Ser Leu Ser Ile Tyr Gly Phe Leu Leu Ile Ala Tyr Leu Leu Val Lys
89      35      40      45
92 Met Ser Leu Ser Phe Phe Tyr Lys Pro Phe Lys Gly Arg Ala Gly Gln
93      50      55      60
96 Tyr Lys Val Ala Ala Ile Ile Pro Ser Tyr Asn Glu Asp Ala Glu Ser
97 65      70      75      80
100 Leu Leu Glu Thr Leu Lys Ser Val Gln Gln Gln Thr Tyr Pro Leu Ala
101      85      90      95
104 Glu Ile Tyr Val Val Asp Asp Gly Ser Ala Asp Glu Thr Gly Ile Lys
105      100      105      110
108 Arg Ile Glu Asp Tyr Val Arg Asp Thr Gly Asp Leu Ser Ser Asn Val
109      115      120      125
112 Ile Val His Arg Ser Glu Lys Asn Gln Gly Lys Arg His Ala Gln Ala
113      130      135      140
116 Trp Ala Phe Glu Arg Ser Asp Ala Asp Val Phe Leu Thr Val Asp Ser
117 145      150      155      160
120 Asp Thr Tyr Ile Tyr Pro Asp Ala Leu Glu Glu Leu Leu Lys Thr Phe
121      165      170      175
124 Asn Asp Pro Thr Val Phe Ala Ala Thr Gly His Leu Asn Val Arg Asn
125      180      185      190
128 Arg Gln Thr Asn Leu Leu Thr Arg Leu Thr Asp Ile Arg Tyr Asp Asn
129      195      200      205
132 Ala Phe Gly Val Glu Arg Ala Ala Gln Ser Val Thr Gly Asn Ile Leu
133      210      215      220
136 Val Cys Ser Gly Pro Leu Ser Val Tyr Arg Arg Glu Val Val Val Pro
137 225      230      235      240
140 Asn Ile Asp Arg Tyr Ile Asn Gln Thr Phe Leu Gly Ile Pro Val Ser
141      245      250      255
144 Ile Gly Asp Asp Arg Cys Leu Thr Asn Tyr Ala Thr Asp Leu Gly Lys
145      260      265      270
148 Thr Val Tyr Gln Ser Thr Ala Lys Cys Ile Thr Asp Val Pro Asp Lys
149      275      280      285
152 Met Ser Thr Tyr Leu Lys Gln Gln Asn Arg Trp Asn Lys Ser Phe Phe
153      290      295      300
156 Arg Glu Ser Ile Ile Ser Val Lys Lys Ile Met Asn Asn Pro Phe Val
157 305      310      315      320
160 Ala Leu Trp Thr Ile Leu Glu Val Ser Met Phe Met Met Leu Val Tyr
161      325      330      335
164 Ser Val Val Asp Phe Phe Val Gly Asn Val Arg Glu Phe Asp Trp Leu
165      340      345      350
168 Arg Val Leu Ala Phe Leu Val Ile Ile Phe Ile Val Ala Leu Cys Arg
169      355      360      365
172 Asn Ile His Tyr Met Leu Lys His Pro Leu Ser Phe Leu Leu Ser Pro
173      370      375      380

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176 Phe Tyr Gly Val Leu His Leu Phe Val Leu Gln Pro Leu Lys Leu Tyr
177 385                      390                      395                      400
180 Ser Leu Phe Thr Ile Arg Asn Ala Asp Trp Gly Thr Arg Lys Lys Leu
181                      405                      410                      415
184 Leu
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189 <211> LENGTH: 22
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Primer sel
196 <400> SEQUENCE: 3
197 gctgatgaga caggtattaa gc                                22
200 <210> SEQ ID NO: 4
201 <211> LENGTH: 20
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Primer se2
208 <400> SEQUENCE: 4
209 atcaaattct ctgacattgc                                20
212 <210> SEQ ID NO: 5
213 <211> LENGTH: 20
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Primer sespl
220 <400> SEQUENCE: 5
221 gactcagata cttatatcta                                20
224 <210> SEQ ID NO: 6
225 <211> LENGTH: 17
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Primer sesp2
232 <400> SEQUENCE: 6
233 tttttacgtg ttcccca                                17
236 <210> SEQ ID NO: 7
237 <211> LENGTH: 1740
238 <212> TYPE: DNA
239 <213> ORGANISM: Paramecium bursaria chlorella virus
241 <400> SEQUENCE: 7
242 aagacttctt gaaagttaca atgggtaaaa atataatcat aatggtttcg tggtagacca    60
244 tcataacttc aaatctaadc gcggttgagg gagcctctct aatcttggct ccggcaatta    120
246 ctgggtatgt tctacattgg aatattgctc tctcgacaat ctggggagta tcagcttatg    180
248 gtattttcgt ttttgggttt ttccttgcaac aagttttatt ttcagaactg aacaggaaac    240
250 gtcttcgcaa gtggatttct ctcagaccta agggttggaa tgatgttcgt ttggctgtga    300
252 tcattgctgg atatcgcgag gatacctata tgttcagaa gtgcctcgag tctgtacgtg    360
254 actctgatta tggcaacggt gcccgctctga tttgtgtgat tgacggtgat gagggacgatg    420

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258 ttgttctgtg tgagtcagac gacaaggaa gtgaacgcat cgactctgat ttctctcgcg 540
260 acatttgtgt cctccagcct catcgtggaa aacgggagtg tctttatact gggtttcaac 600
262 ttgcaaagat ggaccccagt gtcaatgctg tcgttctgat tgacagcgat accgttctcg 660
264 agaaggatgc tattctggaa gttgtatacc cacttgcatg cgatcccag atccaagccg 720
266 ttgcaggatga gtgtaagatt tggaacacag aactctttt gactcttctc gtcgcttggc 780
268 ggtactattc tgcgttttgt gtggagagga gtgccagtc ttttttcagg actgttcagt 840
270 gcgttggggg gccactgggt gcctacaaga ttgatatcat taaggagatt aaggaccct 900
272 ggatttccca gcgctttctt ggtcagaagt gtacttacgg tgacgaccgc cggctaacca 960
274 acgagatcct gatgcgtggt aaaaagggtt gtgtcactcc atttgctgtt ggttggctcg 1020
276 acagtcggac caatgtgttt cggtagatcg ttacgagac ccgctggagt aagtcgtggt 1080
278 gccgcgaaat ttggtacacc ctcttcgcgc cgtggaagca cggtttgtct ggaatttggc 1140
280 tggcctttga atgtttgtat caaattacat acttcttctt cgtgatttac ctcttttctc 1200
282 gcctagccgt tgaggccgac cctcgcgcgc agacagccac ggtgattgtg agcaccacgg 1260
284 ttgcattgat taagtgtggg ttttttcat tccgagccaa ggatattcgg gcgttttact 1320
286 ttgtgcttta tacatttgtt tacttttct gtatgattcc ggccaggatt actgcaatga 1380
288 tgacgctttg ggacattggc tgggggtact gcggtggaag cgagaagcct tccgttggca 1440
290 cccgggtcgc tctgtgggca aagcaatata tcattgcata tatgtggtgg gccgcggtt 1500
292 ttggcgtcgt agtttacagc atcgtccata actggatgtt cgattggaat tctctttctt 1560
294 atcgttttgc tttggttggg atttgttctt acattgtttt tattgttatt gtgctggtgg 1620
296 tttatttcac cggcaaaatt acgacttgga atttcacgaa gcttcagaag gagctaactg 1680
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302 <211> LENGTH: 2937
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304 <213> ORGANISM: Pastuerella Multocida
306 <400> SEQUENCE: 8
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311 gttgaatttc aaattaccaa atgcaaagaa aaactctcag cacatccttc tgttaattca 180
313 gcacatcttt ctgtaaataa agaagaaaaa gtcaatgttt gcgatagtc gtttagatatt 240
315 gcaacacaac tgtaactttc caacgtaaaa aaattagtag tttctgactc ggaaaaaac 300
317 acgttaaaaa ataaatggaa attgtcact gagaagaaat ctgaaaatgc ggaggttaaga 360
319 gcggtcgcgc ttgtaccaa agattttccc aaagatctgg ttttagcgc tttacctgat 420
321 catgttaatg attttacatg gtacaaaaag cgaaagaaa gacttggcat aaaacctgaa 480
323 catcaacatg ttggtctttc tattatcgtt acaacattca atcgaccagc aattttatcg 540
325 attacattag cctgttttagt aaaccaaaaa acacattacc cgtttgaagt tatcgtgaca 600
327 gatgatggta gtcaggaaga tctatcaccg atcattcgcc aatatgaaa taaattggat 660
329 attcgtctacg tcagacaaaa agataacggg tttcaagcca gtgcccgtcg gaatatggga 720
331 ttacgcttag caaaatatga ctttattggc ttactcgact gtgatatggc gccaaatcca 780
333 ttatgggttc attcttatgt tgcagagcta ttagaagatg atgatttaac aatcattggt 840
335 ccaagaaaat acatcgatac acaacatatt gacccaaaa acttcttaaa taacgcgagt 900
337 ttgcttgaat cattaccaga agtgaataacc aataatagtg ttgcccgaag aggggaagga 960
339 acagtttctc tggattggcg cttagaacaa ttcgaaaaaa cagaaaatct ccgcttatcc 1020
341 gattcgcctt tccgtttttt tgcggcgggt aatgttgcct tcgctaaaa atggctaaat 1080
343 aaatccggtt tctttgatga ggaatttaat cactggggtg gagaagatgt ggaatttggg 1140
345 tatcgttat tccgttacgg tagtttcttt aaaactattg atggcattat ggcctaccat 1200
347 caagagccac caggtaaaga aaatgaaacc gatcgtgaag cgggaaaaaa tattacgctc 1260
349 gatattatga gagaaaaggt cccttatatc tatagaaaac ttttaccat agaagattcg 1320

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351 catatcaata gagtaccttt agtttcaatt tatatcccag cttataactg tgcaaaactat 1380
353 attcaacggtt gcgtagatag tgcactgaat cagactggtt ttgatctcga ggtttgatt 1440
355 tgtaacgatg gttcaacaga taatacctta gaagtgatca ataagcttta tggtataaat 1500
357 cctaggggtac gcatcatgtc taaaccaaatt ggcggaatag cctcagcatc aaatgcagcc 1560
359 gtttcttttg ctaaagggtt ttacattggg cagtttagatt cagatgatta tcttgagcct 1620
361 gatgcagttg aactgtgttt aaaagaattt ttaaaagata aaacgctagc ttgtgtttat 1680
363 accactaata gaaacgtcaa tccggatggt agcttaatcg ctaatgggta caattggcca 1740
365 gaattttcac gagaaaaact cacaacggct atgattgctc accactttag aatgttcacg 1800
367 attagagctt ggcatttaac tgatggattc aatgaaaaaa ttgaaaatgc cgtagactat 1860
369 gacatgttcc tcaaactcag tgaagttgga aaatttaaac atcttaataa aatctgctat 1920
371 aaccgtgtat tacatggtga taacacatca attaagaaac ttggcattca aaagaaaaac 1980
373 cattttgttg tagtcaatca gtcattaaat agacaaggca taacttatta taattatgac 2040
375 gaatttgatg atttagatga aagtagaaaag tatattttca ataaaaccgc tgaatatcaa 2100
377 gaagagattg atatcttaaa agatattaaa atcatccaga ataaagatgc caaaatcgca 2160
379 gtcagtattt tttatcccaa tacattaaac ggcttagtga aaaaactaaa caatattatt 2220
381 gaatataata aaaatatatt cgttattggt ctacatgttg ataagaatca tcttacacca 2280
383 gatataaaaa aagaataact agccttctat cataaacatc aagtgaatat tttactaaat 2340
385 aatgatatct catattacac gagtaataga ttaataaaaa ctgaggcgca ttttaagtaat 2400
387 attaataaat taagtcagtt aaatctaaat tgtgaataca tcatttttga taatcatgac 2460
389 agcctattcg ttaaaaatga cagctatgct tatatgaaaa aatatgatgt cggcatgaat 2520
391 ttctcagcat taacacatga ttggatcgag aaaatcaatg cgcattccacc atttaaaaag 2580
393 ctcatataaaa cttattttta tgacaatgac ttaaaaagta tgaatgtgaa aggggcatca 2640
395 caaggtatgt ttatgacgta tgcgctagcg catgagcttc tgacgattat taaagaagtc 2700
397 atcacatctt gccagtcaat tgatagtgtg ccagaatata aactgagga tatttggttc 2760
399 caatttgcac ttttaattctt agaaaagaaa accggccatg tatttaataa aacatcgacc 2820
401 ctgacttata tgccttgga acgaaaatta caatggacaa atgaacaaat tgaaagtgca 2880
403 aaaagaggag aaaatatacc tgtaacaag ttcattatta atagtataac tctataa 2937

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406 &lt;210&gt; SEQ ID NO: 9

407 &lt;211&gt; LENGTH: 972

408 &lt;212&gt; TYPE: PRT

409 <213> ORGANISM: *Pastuerella Multocida*

411 &lt;400&gt; SEQUENCE: 9

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414 1 5 10 15
417 Gln Leu Ala Leu Lys Leu Phe Glu Lys Ser Ala Glu Ile Tyr Gly Arg
418 20 25 30
421 Lys Ile Val Glu Phe Gln Ile Thr Lys Cys Lys Glu Lys Leu Ser Ala
422 35 40 45
425 His Pro Ser Val Asn Ser Ala His Leu Ser Val Asn Lys Glu Glu Lys
426 50 55 60
429 Val Asn Val Cys Asp Ser Pro Leu Asp Ile Ala Thr Gln Leu Leu Leu
430 65 70 75 80
433 Ser Asn Val Lys Lys Leu Val Leu Ser Asp Ser Glu Lys Asn Thr Leu
434 85 90 95
437 Lys Asn Lys Trp Lys Leu Leu Thr Glu Lys Lys Ser Glu Asn Ala Glu
438 100 105 110
441 Val Arg Ala Val Ala Leu Val Pro Lys Asp Phe Pro Lys Asp Leu Val
442 115 120 125
445 Leu Ala Pro Leu Pro Asp His Val Asn Asp Phe Thr Trp Tyr Lys Lys

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VERIFICATION SUMMARY

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